Amendment to the Claims:

Claim 12 (currently amended): A process for producing a diagnostic test ~~diagnostic testing method~~ comprising the steps of:

(i) providing a sample;

(ii) contacting said sample with antisera specific for a Ho-Hi-Ho ~~epitope~~ epitope(s) of contiguous amino acid residues from ~~a polypeptide~~ one of the following polypeptides:IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IFN-α, IFN-β, IFN-65, CD2, CD3,CD4, CD5, CD8, CD11A, CD11b, CD11c, CD16, CD18, CD21, CD28, CD32, CD34, CD35, CD40, CD44, CD45, CD54 CD56, K2, K1, Pβ, Oα, Mα, Mβ2, Mβ1, LMP1, TAP2, LMP7, TAP1, Oβ, IAβ, IAα, IEβ, IEβ2, IEα, CYP21, C4B, CYP21P, C4A, BF, C2, HSP, G7a/b, TNF-α, TNF-β,D,L, Qa, T1a, COL11A2, DPβ2, DPα2, DPβ1, DPα1, DNα, DMα, DM β, DQβ3, DQβ1, DQα1, DRα, DRβ, HSP-70, HLA-B, HLA-C, HLA-X, HLA-E, HLA-J, HLA-A, HLA-H, HLA-G, HLA-F, NGF, somatotropin, somatomedins, parathormone, FSH, LH, EGF, TSH, THS-releasing factor, HGH, GRHR, PDGF, IGF-I, IGF-II, TGF-β, GM-CSF, M-CSF, G-CSF1, erythropoietin, β-HCG, 4-N-acetylgalactosaminyltransferase, GM2, GD2, GD3, MAGE-1, MAGE-2, MAGE-3, MUC-1, MUC-2, MUC-3, MUC-4, MUC-18, ICAM-1, C-CAM, V-CAM, ELAM, NM23, EGFR, E-cadherin, N-CAM, CEA, DCC, PSA, Iler2-neu, UTAA, melanoma antigen p75, K19, HKer 8, pMEL 17, tyrosine related proteins 1 and 2, p97, p53, RB, APC, DCC, NF-1, NF-2, WT-1,

MEN-I, MEN-II, BRCA1, VHL, FCC, MCC, ras, myc, neu, raf, erb, src, fms, jun, trk, ret, gsp, hst, bcl, abil, C1q, C1r, C1s, C4,C2, Factor D, Factor B, properdin, C3, C5, C6, C7, C8, C9, C1Inh, Factor H, C4b-binding protein, DAF, membrane cofactor protein, anaphylatoxin inactivator S protein, HRF,MIRL, CR1, CR2, CR3, CR4, C3a/C4a receptor, HIV (gag, pol, gp41, gp120, vif, tat, rev, nef, vpr, vpu, vpx), HSV (ribonucleotide reductase, α-TIF, ICP4, ICP8, ICP35, LAT-related proteins, gB, gC, gD, gE, gI, gJ), influenza (hemagluttinin, neuroaminidase, PB1, PB2, PA, NP, M_1, M_2, NS_1, NS_2) papillomaviruses (E1, E2, E3, E4, E5a, E5b, E6, E7, E8, L1, L2), adenovirus (E1A, E1B, E2, E3, E4, E5, L1, L2, L3, L4, L5), Epstein-Barr Virus (EBNA), Hepatitis B virus, ($gp27^s$, $gp36^s$, $gp42^s$, $p22^c$, pol, x) and nuclear matrix proteins; wherein said ~~epitope~~ epitope(s) is characterized by a hydrophobic-hydrophilic-hydrophobic motif having an optimal length of amino acid residues determined by a method comprising the steps of :

a) assigning an average hydropathy value to each amino acid of a polypeptide;

b) generating a hydrophilicity plot using the average hydropathy value of each amino acid;

c) fitting a curve segment of the hydrophilicity plot to a negative cosine function, wherein a specific period number value of the negative cosine function equates to the number of amino acids in the curve segment, the period number increasing within a predetermined

chosen period number range after each sequential lagging through the hydrophilicity plot thereby providing fit-correlation values for each curve segment across the linear sequence when using the specific period number value;

d) generating a potential Ho-Hi-Ho epitope set for each specific period number value within the chosen period number value range, wherein each potential Ho-Hi-Ho epitope set contains potential Ho-Hi-Ho epitopes that have a positive fit-correlation value;

e) ranking each potential Ho-Hi-Ho epitope in the potential Ho-Hi-Ho epitope set according to positive fit-correlation values wherein the epitope having highest positive-fit correlation value is ranked number one thereby providing ranked Ho-Hi-Ho potential epitopes for each specific period number value;

f) examining the positioning of at least the highest ranked Ho-Hi-Ho potential epitopes of each set relative to the linear sequence of the plot of step (a) to determine at least one set of Ho-Hi-Ho potential epitopes that exhibit alternating positioning about an equilibrium position wherein the ranking values of the Ho-Hi-Ho potential epitopes coverage towards or diverge away from the equilibrium position; and

g) designating the Ho-Hi-Ho potential epitopes of the optimal set having the most alternating ranking values that either converge or diverge as the immunologically active epitopes which have an

optimal length ~~equating~~ equated to the numeric value of amino acids residues resident in the optimal potential epitope set;

iii) detecting the binding of said antisera to a polypeptide in said sample[[.]] ; and

iv) calculating levels of said polypeptide in said sample indicative of abnormal function due to disease and/or injury.

Claim 19 (currently amended): A process for producing a diagnostic test ~~diagnostic testing method~~ comprising the steps of:

(i) providing a sample;

(ii) contacting said sample with antisera specific for a Ho-Hi-Ho epitope of contiguous amino acid residues from ~~a polypeptide~~ one of the following polypeptides: IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IFN-α, IFN-β, IFN-65, CD2, CD3,CD4, CD5, CD8, CD11A, CD11b, CD11c, CD16, CD18, CD21, CD28, CD32, CD34, CD35, CD40, CD44, CD45, CD54 CD56, K2, K1, Pβ, Oα, Mα, Mβ2, Mβ1, LMP1, TAP2, LMP7, TAP1, Oβ, IAβ, IAα, IEβ, IEβ2, IEα, CYP21, C4B, CYP21P, C4A, BF, C2, HSP, G7a/b, TNF-α, TNF-β,D,L, Qa, T1a, COL11A2, DPβ2, DPα2, DPβ1, DPα1, DNα, DMα, DM β, DQβ3, DQβ1, DQα1, DRα, DRβ, HSP-70, HLA-B, HLA-C, HLA-X, HLA-E, HLA-J, HLA-A, HLA-H, HLA-G, HLA-F, NGF, somatotropin, somatomedins, parathormone, FSH, LH, EGF, TSH, THS-releasing

factor, HGH, GRHR, PDGF, IGF-I, IGF-II, TGF-β, GM-CSF, M-CSF, G-CSF1, erythropoietin, β-HCG, 4-N-acetylgalactosaminyltransferase, GM2, GD2, GD3, MAGE-1, MAGE-2, MAGE-3, MUC-1, MUC-2, MUC-3, MUC-4, MUC-18, ICAM-1, C-CAM, V-CAM, ELAM, NM23, EGFR, E-cadherin, N-CAM, CEA, DCC, PSA, Iler2-neu, UTAA, melanoma antigen p75, K19, HKer 8, pMEL 17, tyrosine related proteins 1 and 2, p97, p53, RB, APC, DCC, NF-1, NF-2, WT-1, MEN-I, MEN-II, BRCA1, VHL, FCC, MCC, ras, myc, neu, raf, erb, src, fms, jun, trk, ret, gsp, hst, bcl, abil, C1q, C1r, C1s, C4,C2, Factor D, Factor B, properdin, C3, C5, C6, C7, C8, C9, C1Inh, Factor H, C4b-binding protein, DAF, membrane cofactor protein, anaphylatoxin inactivator S protein, HRF,MIRL, CR1, CR2, CR3, CR4, C3a/C4a receptor, HIV (gag, pol, qp41, gp120, vif, tat, rev, nef, vpr, vpu, vpx), HSV (ribonucleotide reductase, α-TIF, ICP4, ICP8, ICP35, LAT-related proteins, gB, gC, gD, gE, gI, gJ), influenza (hemagluttinin, neuroaminidase, PB1, PB2, PA, NP, M_1 , M_2 , NS_1, NS_2) papillomaviruses (E1, E2, E3, E4, E5a, E5b, E6, E7, E8, L1, L2), adenovirus (E1A, E1B, E2, E3, E4, E5, L1, L2, L3, L4, L5), Epstein-Barr Virus (EBNA), Hepatitis B virus, ($gp27^s$, $gp36^s$, $gp42^s$, $p22^c$, pol, x) and nuclear matrix proteins; wherein said epitope is characterized by a hydrophobic-hydrophilic-hydrophobic motif having an optimal length of amino acid residues determined by a method comprising the steps of :

(a) fitting a hydrophilicity and/or hydrophobicity plot generated for the amino acid linear sequence of a polypeptide to a mathematically generated continuous curve thereby generating potential epitope sets which include ranked potential epitopes having a specific number of amino acid residues, the mathematically generated curve having at least a maximum positive value;

(b) positioning the ranked potential epitopes for each set on the hydrophilicity and/or hydrophobicity plot to determine the oscillating behavior of the numeric values of ranked potential epitopes; and

(c) deeming the potential epitopes that exhibit the most alternating ~~position~~ either convergent or divergent positioning about an equilibrium position when juxtaposed on the hydrophilicity and/or hydrophobicity plot as the theoretical epitopes and their optimal length corresponds to the specific number of amino acid residues resident in the set of ranked potential ~~epitomes~~ epitopes; and

iii) detecting the binding of said antisera to a polypeptide in said sample[[.]] ; and

iv) calculating levels of said polypeptide in said sample indicative of abnormal function due to disease and/or injury.